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After human genome was sequenced, proteomics has contributed an enormous amount of knowledge on protein structures and functions for drug design and research. The development of mass spectrometry and protein crystallography provide rapidly structural information on target proteins for the drug research.

In this symposium, global analysis of native peptides (peptidome), rapid systematic crystallization and structural analysis of protein crystals, and functional analysis of engineered proteins expressed on the cell surface (combinatorial bioengineering) will be discussed as applied to drug development together with an approach using bioinformatic analysis.